



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:38 PM UTC

PDB ID : 2CQS / pdb_00002cqs
Title : Crystal Structure of Cellvibrio gilvus Cellobiose Phosphorylase Crystallized from Ammonium Sulfate
Authors : Hidaka, M.; Kitaoka, M.; Hayashi, K.; Wakagi, T.; Shoun, H.; Fushinobu, S.
Deposited on : 2005-05-20
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

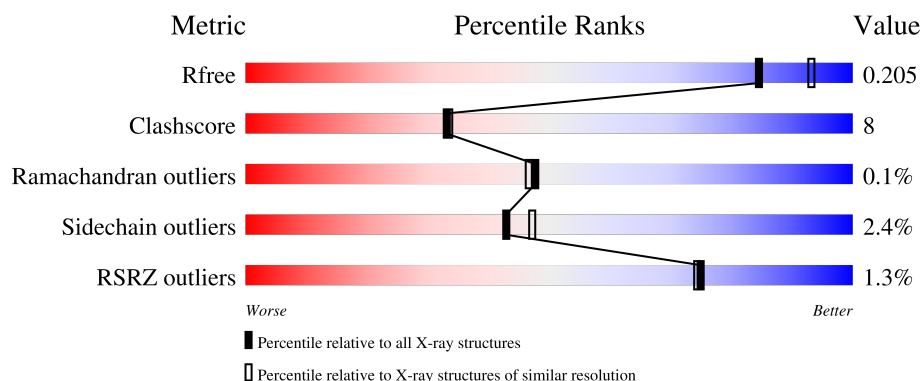
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	842	 80% 16% ..
1	B	842	 2% 78% 19% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13964 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cellobiose Phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	822	Total	C	N	O	S	0	0	0
			6428	4066	1102	1246	14			
1	B	822	Total	C	N	O	S	0	0	0
			6428	4066	1102	1246	14			

There are 40 discrepancies between the modelled and reference sequences:

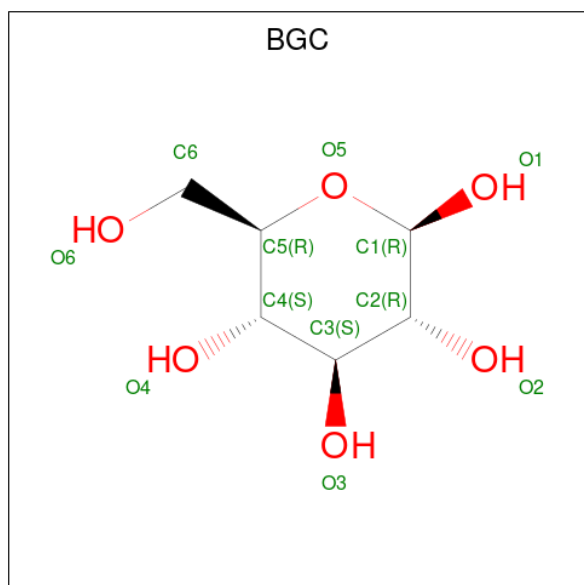
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP O66264
A	-18	GLY	-	expression tag	UNP O66264
A	-17	SER	-	expression tag	UNP O66264
A	-16	SER	-	expression tag	UNP O66264
A	-15	HIS	-	expression tag	UNP O66264
A	-14	HIS	-	expression tag	UNP O66264
A	-13	HIS	-	expression tag	UNP O66264
A	-12	HIS	-	expression tag	UNP O66264
A	-11	HIS	-	expression tag	UNP O66264
A	-10	HIS	-	expression tag	UNP O66264
A	-9	SER	-	expression tag	UNP O66264
A	-8	SER	-	expression tag	UNP O66264
A	-7	GLY	-	expression tag	UNP O66264
A	-6	LEU	-	expression tag	UNP O66264
A	-5	VAL	-	expression tag	UNP O66264
A	-4	PRO	-	expression tag	UNP O66264
A	-3	ARG	-	expression tag	UNP O66264
A	-2	GLY	-	expression tag	UNP O66264
A	-1	SER	-	expression tag	UNP O66264
A	0	HIS	-	expression tag	UNP O66264
B	-19	MET	-	expression tag	UNP O66264
B	-18	GLY	-	expression tag	UNP O66264
B	-17	SER	-	expression tag	UNP O66264
B	-16	SER	-	expression tag	UNP O66264
B	-15	HIS	-	expression tag	UNP O66264

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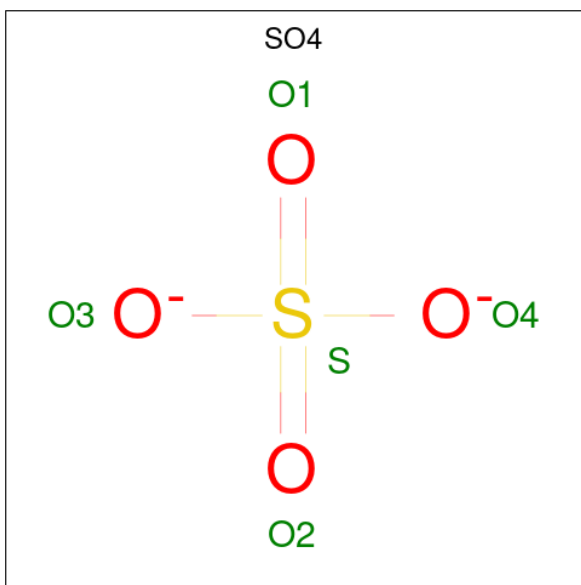
Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP O66264
B	-13	HIS	-	expression tag	UNP O66264
B	-12	HIS	-	expression tag	UNP O66264
B	-11	HIS	-	expression tag	UNP O66264
B	-10	HIS	-	expression tag	UNP O66264
B	-9	SER	-	expression tag	UNP O66264
B	-8	SER	-	expression tag	UNP O66264
B	-7	GLY	-	expression tag	UNP O66264
B	-6	LEU	-	expression tag	UNP O66264
B	-5	VAL	-	expression tag	UNP O66264
B	-4	PRO	-	expression tag	UNP O66264
B	-3	ARG	-	expression tag	UNP O66264
B	-2	GLY	-	expression tag	UNP O66264
B	-1	SER	-	expression tag	UNP O66264
B	0	HIS	-	expression tag	UNP O66264

- Molecule 2 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

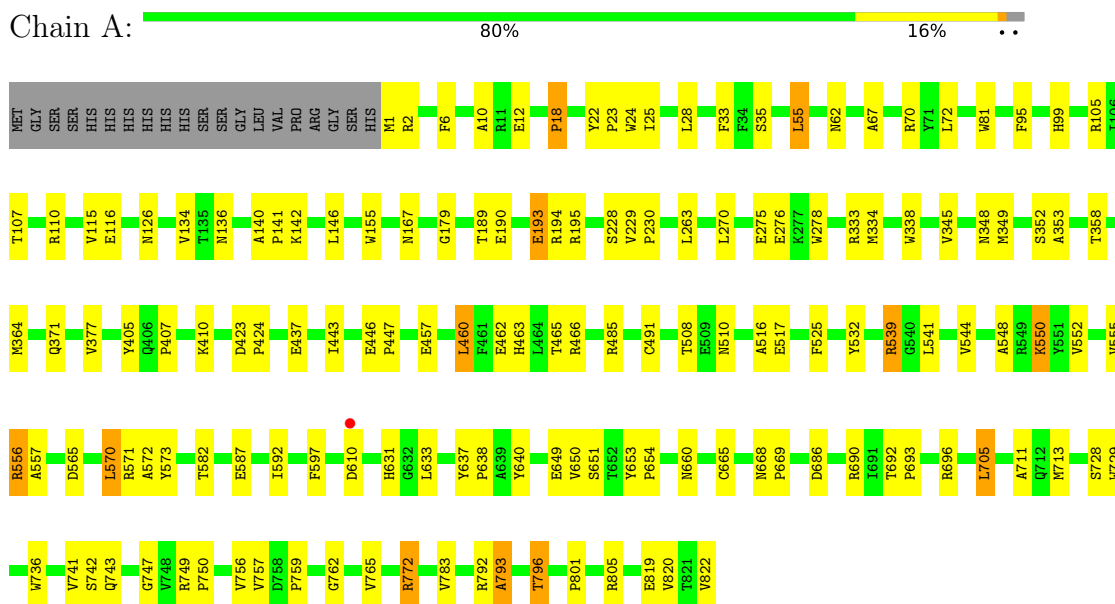
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	529	Total	O	0	0
			529	529		
4	B	545	Total	O	0	0
			545	545		

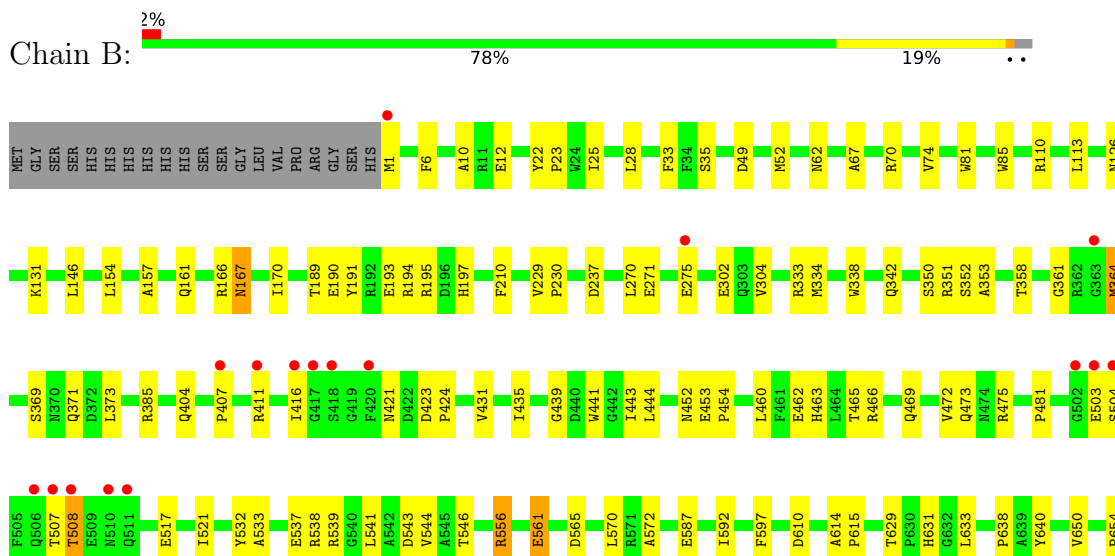
3 Residue-property plots

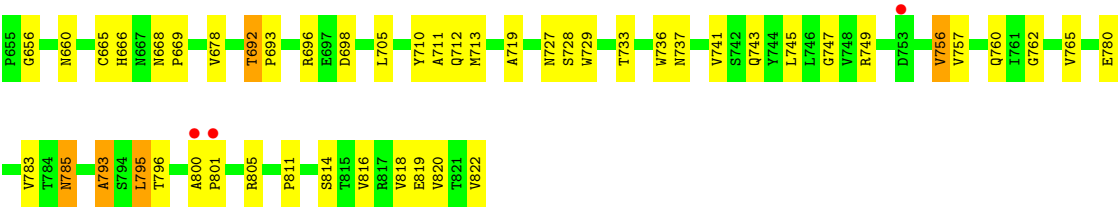
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Cellobiose Phosphorylase



• Molecule 1: Cellobiose Phosphorylase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.84Å 98.42Å 104.04Å 90.00° 102.71° 90.00°	Depositor
Resolution (Å)	49.21 – 2.00 49.21 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.7 (49.21-2.00) 96.8 (49.21-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.176 , 0.213 0.171 , 0.205	Depositor DCC
R_{free} test set	5420 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13964	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.36	0/6604	0.92	21/9009 (0.2%)
1	B	0.37	0/6604	0.93	22/9009 (0.2%)
All	All	0.36	0/13208	0.92	43/18018 (0.2%)

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	TRP	N-CA-C	9.88	122.05	111.28
1	B	338	TRP	N-CA-C	9.34	121.06	111.07
1	A	592	ILE	N-CA-C	8.19	118.99	110.72
1	B	793	ALA	N-CA-C	8.06	121.86	110.50
1	B	592	ILE	N-CA-C	7.90	118.70	110.72
1	B	167	ASN	N-CA-C	7.70	122.11	112.87
1	A	167	ASN	N-CA-C	7.42	121.91	113.01
1	B	191	TYR	N-CA-C	-6.87	103.85	111.82
1	B	194	ARG	N-CA-C	6.76	121.12	113.01
1	A	358	THR	N-CA-C	6.44	120.99	113.20
1	A	25	ILE	N-CA-C	6.36	118.32	109.29
1	A	194	ARG	N-CA-C	6.29	120.55	113.01
1	A	352	SER	N-CA-C	6.20	119.24	111.24
1	B	358	THR	N-CA-C	6.14	120.62	113.20
1	B	25	ILE	N-CA-C	6.02	117.84	109.29
1	A	353	ALA	N-CA-C	6.01	118.24	108.26
1	B	421	ASN	N-CA-C	5.98	120.31	113.19
1	B	352	SER	N-CA-C	5.89	118.84	111.24
1	A	377	VAL	N-CA-C	5.71	117.13	110.62
1	B	747	GLY	N-CA-C	5.71	123.23	115.30
1	A	783	VAL	N-CA-C	5.67	116.11	108.17
1	B	353	ALA	N-CA-C	5.58	117.48	108.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	439	GLY	N-CA-C	-5.57	107.56	115.30
1	A	278	TRP	N-CA-C	5.56	118.54	109.59
1	B	361	GLY	N-CA-C	5.56	119.89	112.77
1	A	654	PRO	N-CA-C	-5.53	105.16	110.47
1	B	783	VAL	N-CA-C	5.49	115.86	108.17
1	B	692	THR	CA-C-N	5.46	126.66	119.84
1	B	692	THR	C-N-CA	5.46	126.66	119.84
1	B	765	VAL	CA-C-N	5.44	125.26	119.28
1	B	765	VAL	C-N-CA	5.44	125.26	119.28
1	B	654	PRO	N-CA-C	-5.43	105.25	110.47
1	B	785	ASN	N-CA-C	5.36	117.25	108.52
1	A	18	PRO	N-CA-C	-5.23	106.91	114.18
1	A	649	GLU	N-CA-C	5.22	117.87	111.82
1	A	228	SER	N-CA-C	5.17	116.60	111.07
1	A	747	GLY	N-CA-C	5.15	122.83	114.90
1	B	795	LEU	N-CA-C	5.12	118.08	110.14
1	A	793	ALA	N-CA-C	5.10	118.03	110.48
1	A	765	VAL	CA-C-N	5.07	124.86	119.28
1	A	765	VAL	C-N-CA	5.07	124.86	119.28
1	A	762	GLY	CA-C-N	5.07	125.14	119.87
1	A	762	GLY	C-N-CA	5.07	125.14	119.87

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6428	0	6071	92	0
1	B	6428	0	6071	104	0
2	A	12	0	12	0	0
2	B	12	0	12	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	529	0	0	7	0
4	B	545	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13964	0	12166	195	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (195) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:504:SER:HB3	1:B:507:THR:HG22	1.48	0.93
1:A:539:ARG:HB3	1:A:539:ARG:HH21	1.35	0.91
1:B:633:LEU:H	1:B:668:ASN:HD21	1.22	0.88
1:A:792:ARG:HB3	1:A:805:ARG:HH11	1.39	0.87
1:B:631:HIS:HD2	1:B:696:ARG:HH12	1.23	0.87
1:A:633:LEU:H	1:A:668:ASN:HD21	1.24	0.84
1:B:342:GLN:HE22	1:B:710:TYR:H	1.25	0.84
1:B:411:ARG:HE	1:B:452:ASN:ND2	1.74	0.84
1:A:796:THR:HG23	1:A:819:GLU:HB3	1.59	0.81
1:A:640:TYR:H	1:A:660:ASN:HD21	1.32	0.77
1:A:631:HIS:HD2	1:A:696:ARG:HH12	1.31	0.76
1:B:631:HIS:CD2	1:B:696:ARG:HH12	2.04	0.76
1:B:640:TYR:H	1:B:660:ASN:HD21	1.34	0.75
1:A:796:THR:CG2	1:A:819:GLU:HB3	2.17	0.74
1:B:503:GLU:HG3	1:B:508:THR:HB	1.71	0.73
1:B:371:GLN:HE21	1:B:736:TRP:HE1	1.37	0.72
1:B:411:ARG:HE	1:B:452:ASN:HD22	1.39	0.71
1:B:465:THR:HG22	1:B:532:TYR:OH	1.90	0.71
1:B:503:GLU:CG	1:B:508:THR:HB	2.22	0.70
1:A:539:ARG:HH21	1:A:539:ARG:CB	2.05	0.69
1:A:465:THR:HG21	4:A:2174:HOH:O	1.91	0.69
1:B:350:SER:HB3	1:B:364:MET:HE2	1.76	0.68
1:A:517:GLU:O	1:A:572:ALA:HB1	1.94	0.67
1:A:371:GLN:NE2	1:A:736:TRP:HE1	1.92	0.67
1:A:371:GLN:HE21	1:A:736:TRP:HE1	1.40	0.67
1:B:465:THR:HG21	4:B:3260:HOH:O	1.94	0.66
1:B:533:ALA:O	1:B:537:GLU:HG3	1.95	0.65
1:B:49:ASP:OD2	1:B:407:PRO:HG2	1.98	0.64
1:B:561:GLU:HG3	4:B:3312:HOH:O	1.99	0.62
1:A:631:HIS:CD2	1:A:696:ARG:HH12	2.15	0.61
1:A:437:GLU:OE1	1:A:772:ARG:NH2	2.33	0.61
1:B:587:GLU:HA	1:B:638:PRO:HG2	1.80	0.61
1:B:6:PHE:CG	1:B:333:ARG:HD3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:517:GLU:O	1:B:572:ALA:HB1	2.01	0.60
1:A:465:THR:HG22	1:A:532:TYR:OH	2.01	0.60
1:A:443:ILE:HG12	1:A:460:LEU:HD12	1.83	0.60
1:B:74:VAL:HG22	1:B:146:LEU:HD22	1.83	0.60
1:B:743:GLN:HB3	1:B:749:ARG:HB3	1.83	0.60
1:B:350:SER:CB	1:B:364:MET:HE2	2.30	0.60
1:B:793:ALA:HB2	1:B:822:VAL:HG22	1.84	0.59
1:B:411:ARG:NE	1:B:452:ASN:ND2	2.50	0.59
1:A:6:PHE:CG	1:A:333:ARG:HD3	2.39	0.58
1:B:796:THR:HA	1:B:801:PRO:HA	1.86	0.56
1:A:485:ARG:NH2	1:A:508:THR:O	2.37	0.56
1:A:1:MET:HE3	1:A:2:ARG:O	2.05	0.56
1:A:743:GLN:HB3	1:A:749:ARG:HB3	1.87	0.56
1:B:469:GLN:O	1:B:472:VAL:HG22	2.06	0.56
1:A:229:VAL:HB	1:A:230:PRO:HD3	1.87	0.56
1:B:504:SER:O	1:B:508:THR:HG22	2.06	0.56
1:B:504:SER:HB3	1:B:507:THR:CG2	2.30	0.55
1:B:385:ARG:HG3	1:B:443:ILE:HD12	1.89	0.55
1:A:189:THR:HG22	1:A:190:GLU:HG3	1.88	0.54
1:A:796:THR:HG23	1:A:819:GLU:CB	2.34	0.54
1:B:62:ASN:ND2	1:B:67:ALA:HB3	2.22	0.54
1:A:28:LEU:HB2	1:A:35:SER:HB2	1.90	0.54
1:A:81:TRP:CG	1:A:110:ARG:HD3	2.43	0.53
1:A:565:ASP:HB2	1:A:570:LEU:HD13	1.89	0.53
1:A:793:ALA:HB2	1:A:822:VAL:HG22	1.89	0.53
1:B:52:MET:HE3	4:B:3077:HOH:O	2.08	0.53
1:B:633:LEU:H	1:B:668:ASN:ND2	2.00	0.52
1:A:55:LEU:HD22	1:A:155:TRP:CZ3	2.45	0.52
1:A:516:ALA:HA	1:A:573:TYR:O	2.10	0.52
1:B:460:LEU:O	1:B:463:HIS:HB2	2.10	0.52
1:A:72:LEU:HD23	1:A:115:VAL:HG11	1.93	0.51
1:B:1:MET:HG3	1:B:698:ASP:O	2.10	0.51
1:B:481:PRO:HG2	1:B:521:ILE:HB	1.92	0.51
1:B:795:LEU:HD22	1:B:820:VAL:HG22	1.91	0.51
1:B:472:VAL:HG23	1:B:473:GLN:HG3	1.93	0.51
1:B:371:GLN:NE2	1:B:736:TRP:HE1	2.08	0.51
1:A:134:VAL:HG21	1:A:146:LEU:HD11	1.93	0.50
1:B:189:THR:HG22	1:B:190:GLU:HG3	1.91	0.50
1:A:55:LEU:HD22	1:A:155:TRP:HZ3	1.75	0.50
1:A:136:ASN:ND2	1:A:142:LYS:HG2	2.26	0.50
1:A:364:MET:HG2	1:A:407:PRO:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:431:VAL:O	1:B:435:ILE:HG12	2.13	0.49
4:A:2132:HOH:O	1:B:190:GLU:HA	2.13	0.48
1:B:796:THR:OG1	1:B:819:GLU:HB3	2.13	0.48
1:A:423:ASP:HB2	1:A:424:PRO:HD3	1.95	0.48
1:A:539:ARG:HH21	1:A:539:ARG:CG	2.24	0.48
1:A:22:TYR:CD2	1:A:23:PRO:HD2	2.48	0.48
1:A:550:LYS:NZ	1:A:550:LYS:HB3	2.29	0.48
1:A:105:ARG:HD2	4:A:2369:HOH:O	2.14	0.47
1:B:334:MET:HE2	1:B:693:PRO:HD2	1.96	0.47
1:B:441:TRP:CH2	1:B:538:ARG:HG3	2.49	0.47
1:A:348:ASN:C	1:A:349:MET:HE2	2.39	0.47
1:A:62:ASN:ND2	1:A:67:ALA:HB3	2.29	0.47
1:A:334:MET:HG3	1:A:692:THR:CG2	2.44	0.47
1:A:741:VAL:HG13	1:A:742:SER:N	2.29	0.47
1:A:457:GLU:H	1:A:457:GLU:CD	2.23	0.47
1:B:404:GLN:NE2	1:B:416:ILE:HG12	2.30	0.47
1:B:469:GLN:NE2	1:B:472:VAL:HG21	2.29	0.47
1:B:157:ALA:O	1:B:161:GLN:HG3	2.15	0.47
1:A:263:LEU:HD23	4:A:2133:HOH:O	2.13	0.46
1:A:792:ARG:HB3	1:A:805:ARG:NH1	2.20	0.46
1:A:541:LEU:HB3	1:A:544:VAL:HB	1.96	0.46
1:B:541:LEU:HB3	1:B:544:VAL:HB	1.96	0.46
1:B:444:LEU:HD13	1:B:539:ARG:HD2	1.96	0.46
1:A:650:VAL:HG13	1:A:651:SER:N	2.30	0.46
1:A:796:THR:HA	1:A:801:PRO:HA	1.96	0.46
1:A:460:LEU:O	1:A:463:HIS:HB2	2.16	0.46
1:B:334:MET:HG3	1:B:692:THR:CG2	2.46	0.46
1:A:749:ARG:HG3	1:A:756:VAL:HB	1.98	0.46
1:B:81:TRP:CG	1:B:110:ARG:HD3	2.51	0.46
1:A:587:GLU:HA	1:A:638:PRO:HD2	1.97	0.46
1:B:757:VAL:HG11	1:B:820:VAL:HG21	1.98	0.46
1:B:6:PHE:CD1	1:B:333:ARG:HD3	2.50	0.46
1:A:18:PRO:HG3	1:A:95:PHE:CD2	2.52	0.45
1:A:548:ALA:O	1:A:552:VAL:HG23	2.17	0.45
1:A:70:ARG:HD2	1:A:70:ARG:H	1.81	0.45
1:B:33:PHE:HB2	1:B:126:ASN:HD22	1.80	0.45
1:B:154:LEU:CD1	1:B:167:ASN:HB2	2.47	0.45
1:B:711:ALA:HA	1:B:728:SER:HA	1.97	0.45
1:B:756:VAL:HA	1:B:805:ARG:O	2.16	0.45
1:B:760:GLN:NE2	4:B:3208:HOH:O	2.49	0.45
1:A:571:ARG:O	1:A:572:ALA:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:CYS:O	1:A:669:PRO:HD3	2.17	0.45
1:A:33:PHE:HB2	1:A:126:ASN:HD22	1.82	0.44
1:B:22:TYR:CD2	1:B:23:PRO:HD2	2.53	0.44
1:A:556:ARG:HG3	1:A:557:ALA:N	2.32	0.44
1:A:711:ALA:HA	1:A:728:SER:HA	1.98	0.44
1:B:270:LEU:HD22	1:B:270:LEU:N	2.33	0.44
1:B:350:SER:C	1:B:351:ARG:HH11	2.25	0.44
1:A:462:GLU:O	1:A:466:ARG:HG2	2.17	0.44
1:B:210:PHE:O	1:B:237:ASP:HA	2.18	0.44
1:A:70:ARG:HD2	1:A:70:ARG:N	2.33	0.44
1:B:10:ALA:O	1:B:12:GLU:HG3	2.18	0.44
1:A:10:ALA:O	1:A:12:GLU:HG3	2.18	0.43
1:A:525:PHE:CD1	1:A:555:VAL:HG21	2.53	0.43
1:B:131:LYS:HB2	1:B:304:VAL:HG11	1.99	0.43
1:B:666:HIS:O	1:B:669:PRO:HD2	2.17	0.43
1:B:556:ARG:HG2	1:B:556:ARG:HH21	1.82	0.43
1:B:167:ASN:HA	1:B:170:ILE:HG12	1.99	0.43
1:B:692:THR:HG23	1:B:693:PRO:HD2	2.00	0.43
1:A:796:THR:HG22	4:A:2293:HOH:O	2.18	0.43
1:B:70:ARG:HD2	1:B:70:ARG:H	1.84	0.43
1:A:650:VAL:O	1:A:660:ASN:HB2	2.18	0.43
1:B:650:VAL:O	1:B:660:ASN:HB2	2.18	0.43
1:A:405:TYR:CD1	1:A:410:LYS:HA	2.54	0.43
1:B:795:LEU:CD2	1:B:820:VAL:HG22	2.48	0.43
1:A:24:TRP:O	1:A:99:HIS:HE1	2.00	0.43
1:A:6:PHE:CD1	1:A:333:ARG:HD3	2.54	0.42
1:A:275:GLU:HG2	4:A:2362:HOH:O	2.18	0.42
1:B:369:SER:O	1:B:373:LEU:HG	2.18	0.42
1:B:614:ALA:HA	1:B:615:PRO:HD3	1.87	0.42
1:A:491:CYS:HB3	1:A:650:VAL:N	2.34	0.42
1:A:692:THR:HA	1:A:693:PRO:HD3	1.89	0.42
1:A:757:VAL:HG11	1:A:820:VAL:HG21	2.01	0.42
1:B:462:GLU:O	1:B:466:ARG:HG2	2.20	0.42
1:B:728:SER:O	1:B:729:TRP:HB2	2.18	0.42
1:A:759:PRO:HB2	1:A:822:VAL:HG21	2.01	0.42
1:B:302:GLU:H	1:B:302:GLU:CD	2.28	0.42
1:A:190:GLU:O	1:A:193:GLU:HG3	2.19	0.42
1:B:668:ASN:N	1:B:669:PRO:CD	2.83	0.42
1:B:475:ARG:HA	1:B:481:PRO:HA	2.01	0.42
1:B:811:PRO:HG2	1:B:814:SER:OG	2.20	0.42
1:A:179:GLY:HA3	4:A:2051:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:ALA:HB1	1:A:141:PRO:HD2	2.02	0.41
1:B:190:GLU:HB2	1:B:195:ARG:HD2	2.02	0.41
1:B:229:VAL:HB	1:B:230:PRO:HD3	2.01	0.41
1:B:678:VAL:O	1:B:678:VAL:HG12	2.20	0.41
1:B:743:GLN:CB	1:B:749:ARG:HB3	2.48	0.41
1:A:705:LEU:HD23	1:A:728:SER:HB3	2.02	0.41
1:B:423:ASP:HB2	1:B:424:PRO:HD3	2.02	0.41
1:B:70:ARG:HD2	1:B:70:ARG:N	2.34	0.41
1:B:453:GLU:HA	1:B:454:PRO:HD3	1.89	0.41
1:A:446:GLU:HA	1:A:447:PRO:HD3	1.92	0.41
1:B:665:CYS:O	1:B:669:PRO:HD3	2.21	0.41
1:B:692:THR:HA	1:B:693:PRO:HD3	1.85	0.41
1:B:800:ALA:HA	1:B:801:PRO:HD2	1.94	0.41
1:B:565:ASP:HB2	1:B:570:LEU:HD13	2.03	0.41
1:B:741:VAL:HA	1:B:745:LEU:HD12	2.02	0.41
1:B:749:ARG:CG	1:B:756:VAL:HG22	2.51	0.41
1:A:190:GLU:HA	4:B:3083:HOH:O	2.21	0.41
1:A:190:GLU:HB2	1:A:195:ARG:HD2	2.03	0.41
1:A:270:LEU:N	1:A:270:LEU:HD22	2.36	0.41
1:A:637:TYR:CD1	1:A:638:PRO:HA	2.56	0.41
1:A:653:TYR:OH	1:B:166:ARG:HG3	2.21	0.41
1:A:686:ASP:O	1:A:690:ARG:HG3	2.20	0.41
1:A:749:ARG:HA	1:A:750:PRO:HD3	1.80	0.41
1:B:411:ARG:NE	1:B:452:ASN:HD22	2.12	0.41
1:A:345:VAL:HG21	1:A:729:TRP:CZ3	2.56	0.41
1:B:28:LEU:HB2	1:B:35:SER:HB2	2.02	0.41
1:B:733:THR:O	1:B:737:ASN:HB2	2.21	0.41
1:A:668:ASN:N	1:A:669:PRO:CD	2.84	0.40
1:B:62:ASN:HD22	1:B:67:ALA:HB3	1.85	0.40
1:B:197:HIS:HB3	1:B:271:GLU:HG2	2.03	0.40
1:B:656:GLY:HA3	1:B:719:ALA:HB2	2.03	0.40
1:A:485:ARG:HA	1:A:510:ASN:ND2	2.37	0.40
1:A:539:ARG:CG	1:A:539:ARG:NH2	2.84	0.40
1:A:570:LEU:HD12	1:A:570:LEU:HA	1.96	0.40
1:B:712:GLN:HB3	1:B:727:ASN:HB2	2.03	0.40
1:A:107:THR:OG1	1:A:116:GLU:HG3	2.20	0.40
1:B:631:HIS:HD2	1:B:696:ARG:NH1	2.05	0.40
1:B:780:GLU:HA	1:B:780:GLU:OE1	2.21	0.40
1:B:762:GLY:O	1:B:785:ASN:ND2	2.47	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	820/842 (97%)	781 (95%)	39 (5%)	0	100	100
1	B	820/842 (97%)	773 (94%)	46 (6%)	1 (0%)	48	46
All	All	1640/1684 (97%)	1554 (95%)	85 (5%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	85	TRP

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	665/682 (98%)	650 (98%)	15 (2%)	44	49
1	B	665/682 (98%)	648 (97%)	17 (3%)	40	44
All	All	1330/1364 (98%)	1298 (98%)	32 (2%)	43	47

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	LEU
1	A	193	GLU
1	A	276	GLU
1	A	460	LEU
1	A	539	ARG

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Mol	Chain	Res	Type
1	A	550	LYS
1	A	556	ARG
1	A	570	LEU
1	A	582	THR
1	A	597	PHE
1	A	610	ASP
1	A	705	LEU
1	A	713	MET
1	A	772	ARG
1	A	796	THR
1	B	113	LEU
1	B	193	GLU
1	B	275	GLU
1	B	364	MET
1	B	508	THR
1	B	543	ASP
1	B	546	THR
1	B	556	ARG
1	B	561	GLU
1	B	597	PHE
1	B	610	ASP
1	B	629	THR
1	B	705	LEU
1	B	713	MET
1	B	756	VAL
1	B	816	VAL
1	B	818	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	99	HIS
1	A	126	ASN
1	A	130	GLN
1	A	158	GLN
1	A	161	GLN
1	A	256	GLN
1	A	317	ASN
1	A	371	GLN
1	A	414	ASN
1	A	578	ASN

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Mol	Chain	Res	Type
1	A	631	HIS
1	A	644	GLN
1	A	660	ASN
1	A	668	ASN
1	A	727	ASN
1	A	743	GLN
1	A	760	GLN
1	B	19	HIS
1	B	62	ASN
1	B	126	ASN
1	B	130	GLN
1	B	161	GLN
1	B	284	GLN
1	B	342	GLN
1	B	371	GLN
1	B	395	GLN
1	B	406	GLN
1	B	452	ASN
1	B	469	GLN
1	B	473	GLN
1	B	510	ASN
1	B	578	ASN
1	B	631	HIS
1	B	644	GLN
1	B	660	ASN
1	B	668	ASN
1	B	737	ASN
1	B	760	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	B	2902	-	4,4,4	0.29	0	6,6,6	0.12	0
2	BGC	B	2901	-	12,12,12	0.41	0	17,17,17	0.39	0
3	SO4	A	1902	-	4,4,4	0.36	0	6,6,6	0.07	0
2	BGC	A	1901	-	12,12,12	0.39	0	17,17,17	0.37	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	B	2901	-	-	0/2/22/22	0/1/1/1
2	BGC	A	1901	-	-	1/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1901	BGC	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	822/842 (97%)	-0.23	1 (0%) 92 91	13, 22, 36, 52	0
1	B	822/842 (97%)	-0.15	20 (2%) 59 59	13, 22, 40, 61	0
All	All	1644/1684 (97%)	-0.19	21 (1%) 75 74	13, 22, 38, 61	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	502	GLY	4.8
1	B	507	THR	4.6
1	B	417	GLY	4.1
1	B	510	ASN	3.8
1	B	416	ILE	3.4
1	B	508	THR	3.2
1	B	511	GLN	3.2
1	B	418	SER	3.2
1	B	1	MET	3.2
1	B	407	PRO	2.9
1	A	610	ASP	2.8
1	B	506	GLN	2.7
1	B	411	ARG	2.6
1	B	363	GLY	2.5
1	B	504	SER	2.4
1	B	503	GLU	2.3
1	B	801	PRO	2.3
1	B	275	GLU	2.2
1	B	420	PHE	2.1
1	B	800	ALA	2.1
1	B	753	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGC	B	2901	12/12	0.88	0.10	25,30,34,35	0
2	BGC	A	1901	12/12	0.94	0.07	20,23,25,26	0
3	SO4	B	2902	5/5	0.97	0.05	22,23,25,27	0
3	SO4	A	1902	5/5	0.99	0.04	23,24,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.